

-2901 LMO2COM/MYOD
 ACAGGGCATGGTGGCAGGTGCCTGTAAATCTCAGTTACTCGGGAGGTGGAGGTTGCAATGA

-2841 AEF1 S8/
 GCCCAGATCGCACCAATTGCACTCCAGCCTGGGCAACAAAAGGTGAAACTCCATCTCAATT

-2781
 NKX2.5
AAAAAAAAAGAATGATTTGGTGGTCACTCAAATAGGTAGGAGAAGAAGGAGAGAGG

-2721 S8 GATA
 AGATGGAGGGTCAGGGAGATCTAATTACTCTCTAAAATCATGCTAGGAAAGATAACACCT

-2661
 TTTAATAACACTCTGCTTTATAACATCATTCTGCCAAGGAGCTCAAAGGTTCAACA

-2601
 AAGTTCACTTTCAGAAAACCCTTGAGGAAGACAGAATATAACATCTCTCCATTAA

-2541 IK2 LYF1
 AAGATGAAGAACAGGCCGGGCACAATGGCTAATGCCGTAAATCCCAGCACTTGGGAGG

-2481
 CTGAGGCCAGAGGATCGCTTGAGCTCCAGAGTTGAGACCAGCCTGGATAACATGGCAAA

-2421 LMO2COM/MYOD/ AEF1
 ACCCTGTCTCTACAAAAAAAATACAAAAATTAGATGGGTGTGGTGGATGCACCTGTGGT

-2361 LYF1 AEF1 NKX2.5
 CCCAGCTACTTGGGAGGCTAAGGTGGAGGATCGCTTGAGCCCAGGGAGTCAAGTCTACA

-2301 NFY/CAAT
 CTGAGCCATGATTGGATCACTGCACTCCAGCCTGGTAGACAGAGCAAGACCTGTCTCAA

-2241 MZF1
 AAAAAAGAAATGAAAGAGAAAGAAAGAGAGGGAGAGGAGAGGAGTGAGGGGAGGAGG

-2181 MZF1 HFH2/SRY/
GAGGGGGGGAGGAAGGAAGGAAGGAAGGAAAGGAAAAAAAGATGAAAAAGAAAAAAACA

-2121 EVI1 CREBPI/VBP NKX2.5
AGATGAAACAGAGGCAGAAAGACTTACGTAAATTGCTCATCATGTGGTTGTCAAGTTG

-2061
 CCCCCAAAACCCAAATTATTGACCAAGGTTATTCTTGACTGAGGCAAGGGGTCCGCTCT

-2001
 CCTGGGCCTGGCTTAGAAAGCTCATCTGCCTTCTGAGATCCATCCCTTCTT

Figure 1

-1941 TTATTTCTTGACACGGAGTCTGCTCTGCACTCAGGCTGGAGTGCAGTGGCATGATC

-1881 TCGACTCACTGTAACCTCTGCCTCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGA

-1821 GATA GATAACAGG CGCCCGCCACCATCTGGCTAATTTGTATTTAGTAAAGACTGGGTT

-1761 TCATCATGTTGCCAGGTTGGTT LXR α /AEF1 TCGA AEF1/
ACTCCTGACCTGAGGTGAGCT GCCCACCTTGGC

-1701 LYF1/IK2 CTCCCCAAAG TGCTGGGATTACAGGCATGAGCCACTGCGCCCAGCTCAGATCCATCCCTT

-1641 CTAAGGGCAAACAGTCCATGGTGCAAAGGGGCATGCCACCCAGAGTTATGAGTACCTGG

-1581 GACTCCAGAATTCTTGCTGGTGGCCTCCACATGCACTTCCAGGGCCTGCTTGGCCTC

-1521 TTCTATGCGTCTGCTGAGTGTGATAGAACCACTGATGTGAGTACCTGGCTTGAGCC

-1461 GTGGCCTGGAGATCCTGTTGACTGTAGCATGGAGGGGGCTTGTGCAGCTGA ATGTCTGCA AP4 LMO2-

-1401 COM/MYOD/ AEF1/E47 ZID/AEF1 TGCAGGTGGTGGAG TTGAATATGATGGAGCTGGAGGTGGGA AGAGAAGTAGGCTTG

-1341 GGGCAGCTCTCATGCCACCTCATTCTGCCAAAACTCAGGTCAA AACTGTGAAGAGTCT AEF1

-1281 PPAR PPAR AAATGTGAATC TGCCTTCAAGGTGGCTACAAAGGTATTTGTCAAGGTAGGAGACCTT

-1221 USF/NMYC/MYCMAX GTGGCCTCCACGTGCA TCCAGGGCCTGCTTGGCCTCTTACGGGTCTGCTGAGT

-1161 CTTCTATGAATCCTCAGGGCAGATTCAATTAGACTCTCACAGTTTGACCTG AEF1

-1101 AGTTTGGCCAGA AATAGGTGACATTAGTTGTTGGCTTGATGGATGACTAAATATT AP1

-1041 AGACATGGTGTAGGCCTGCATTCTACTCTTGCTTTTTGCCCCCTCCAGTGT

-981 TGGGTAGTTTGCT CCCCTACAGCCA AAGGCAAACAGAGAA GTTGGAGGTCTGGAGTGG HNF3 β

Figure 1 (Suite 1)

-921 NKX2.5 PPAR/NKX2.5/PPAR
CTACATAATTTACACGACTGCAATTCTCTGGCTGCACTCAAATGTATACAAACTAA

-861 GATA
ATACAAGTCCTGTGTTTTATCACAGGGAGGCTGATCAATATAATGAAATTAAAAGGGGG

-801 SOX5 SRY/HFH/HNF3 β SRY/HFH/HNF3 β
CTGGTCCATATTGTTCTGTGTTTTTGTTGTTGTTGTTCTTTTGTTTT

-741
TGTGGCCTCCTCCTCTCAATTTATGAAGAGAACAGTAAGATGTTCTCTCGGGTCCTC

-681 MZF1 IK2/NF κ B/CREL LMO2COM/GATA
TGAGGGACCTGGGGAGCTCAGGCTGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAAAAAT

-621 MZF1/SRY PPAR PPAR
CAAAGTCCAGGTTGTGGGGGGAAAACAAAAGCAGCCCTTACCCAGAGGACTGTCCGCC

-561 MZF1 HNF3 β /SRY/EVI1
TCCCCCTCACCCCAGCCTAGGCCTTGAAAGGAAACAAAAGACAAGACAAAATGATTGGC

-501 MZF1 AP4
GTCCTGAGGGAGATTCAGCCTAGAGCTCTCTCCCCCAATCCCTCCTCCGGCTGAGGA

-441 SRY STAT
AACTAACAAAGGAAAAAAAATTGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGG

-381 STAT/PPAR PPAR
TGCCCTTGGTGCCGGGAACGGGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGC

-321 AP2 MZF1
TTCCCGCGCGTCTAGGCCGGCGGGCGGGCGGGGGAAGGGGACGCAGACCGCGGACCC

-261 LMO2COM/MYOD/ E47 RREB1 MZF1/
TAAGACACCTGCTGACCCCTCCCCCCCACCCACCCACCCACCTCCCCCAACTCCCT

-201 CMYB SP1/GC USF/NMYC/
AGATGTGTCGTGGCGGCTGAAACGTGCCCCGTTAAGGGGCGGGCCCGGCTCCACGTGC

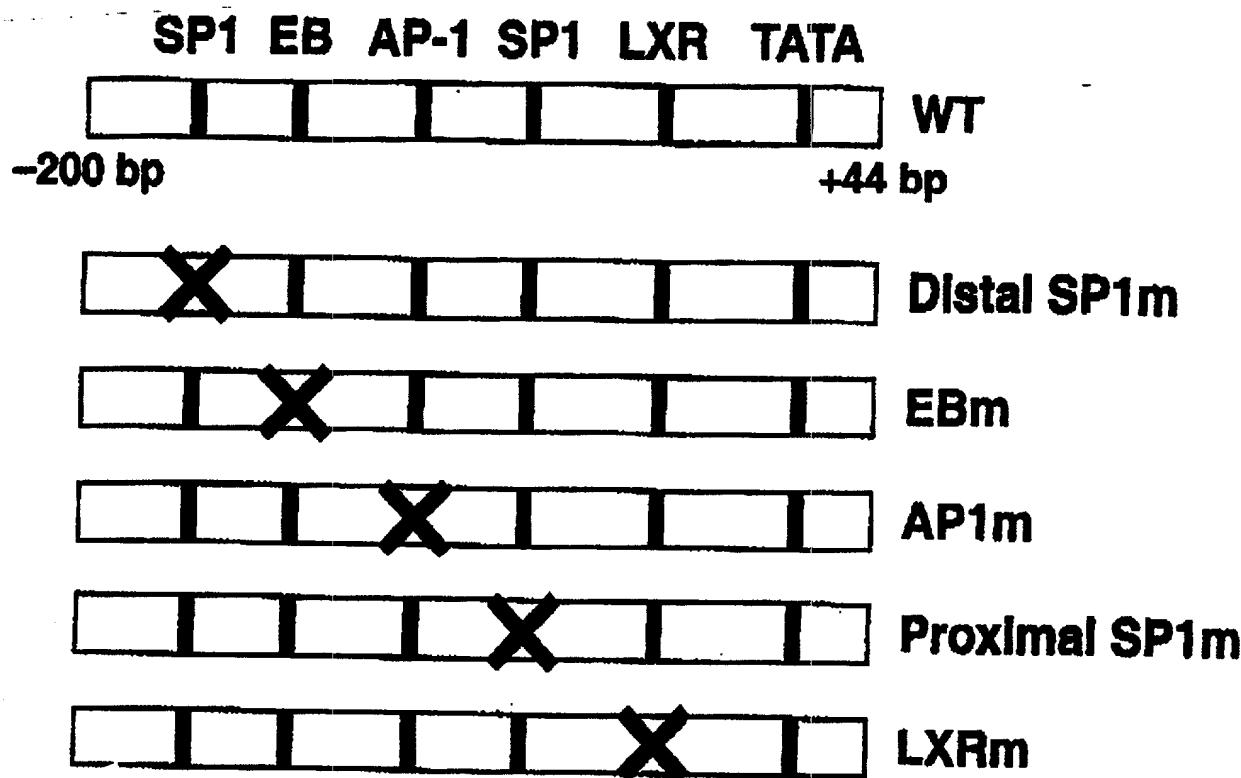
-141 ARNT NFE2/AP1 XFD1/HFH GC/SP1/MZF1
TTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAAGGGGGCGGGAGGAGGGAG

-81 TATA
AGCACAGGTTGACCGATAGTAACCTTGCGCTCGGTGCAGCCGAATTCTATAAAAGGAA

-21 +1
CTAGTCCCGGAAAAACCCCTAATTGCGAGCGAGAG

Figure 1 (suite 2)

FIGURE 2A



0 50 100 150 200 250 300 350

FIGURE 2B

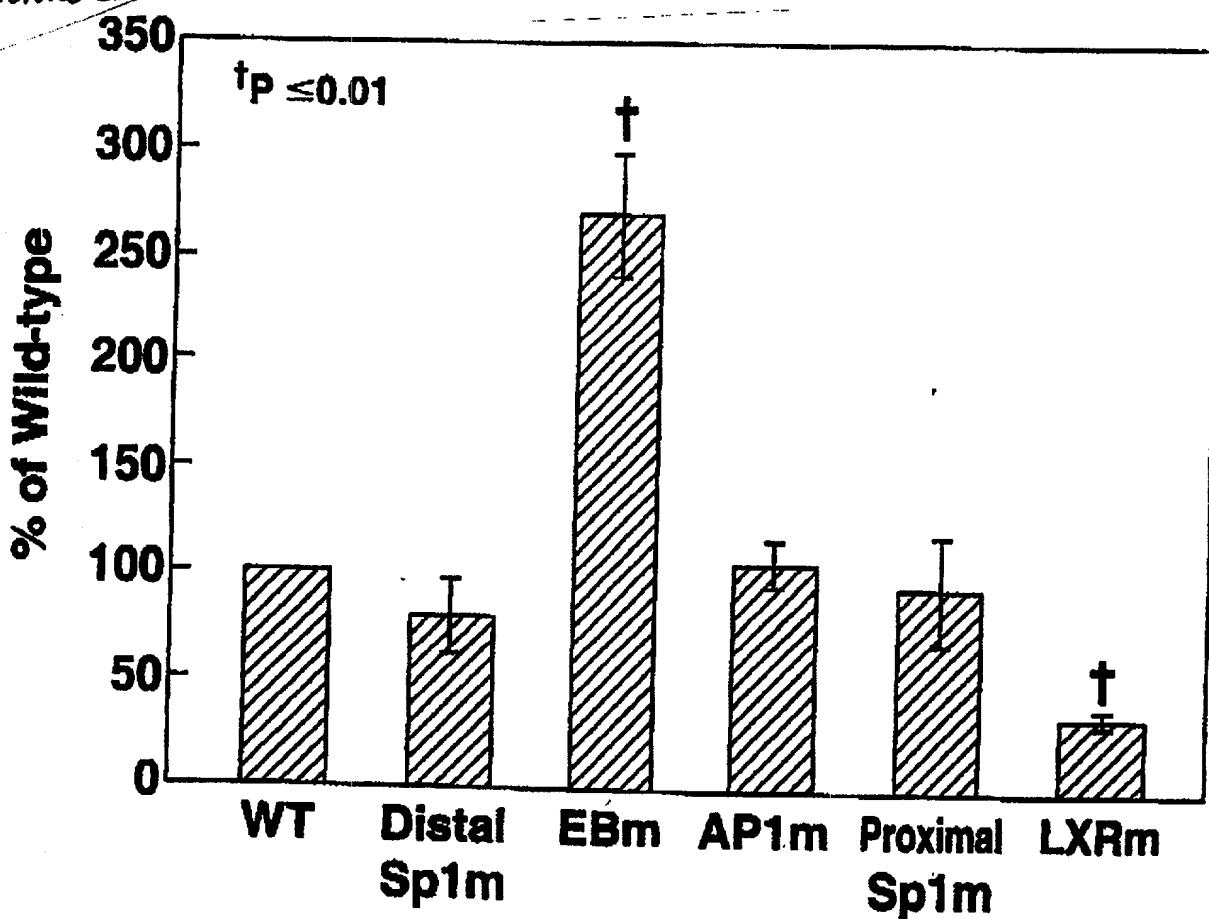
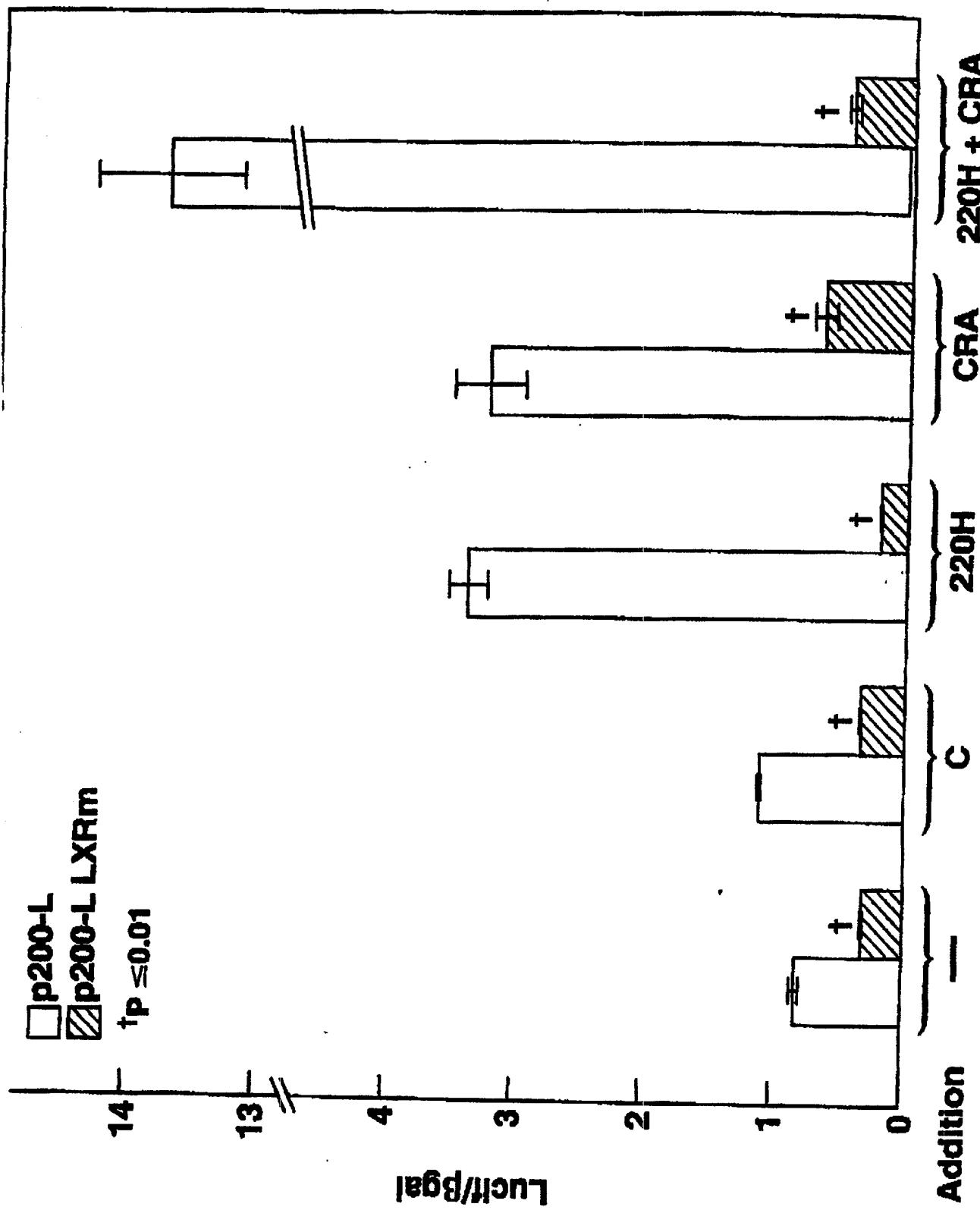


FIGURE 3



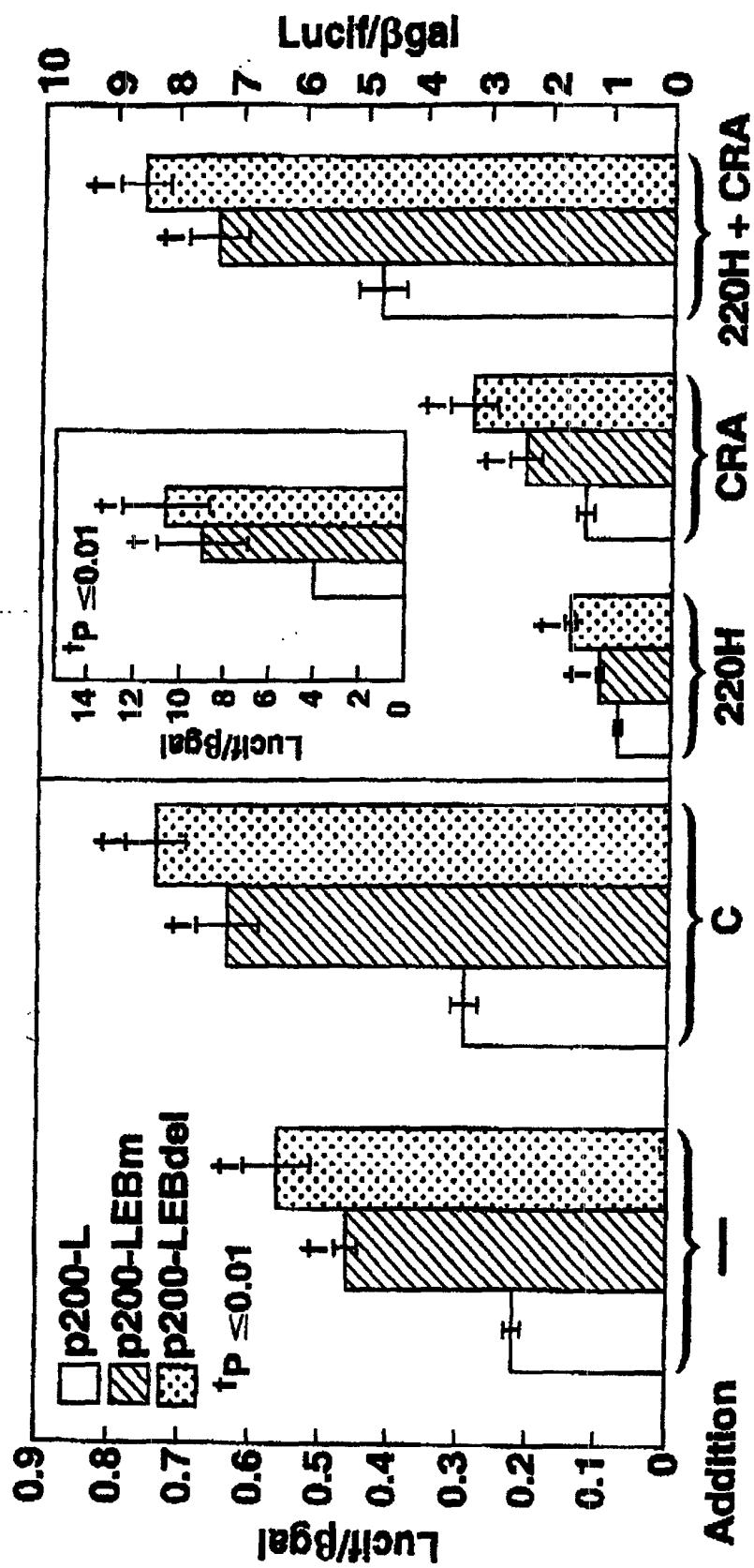
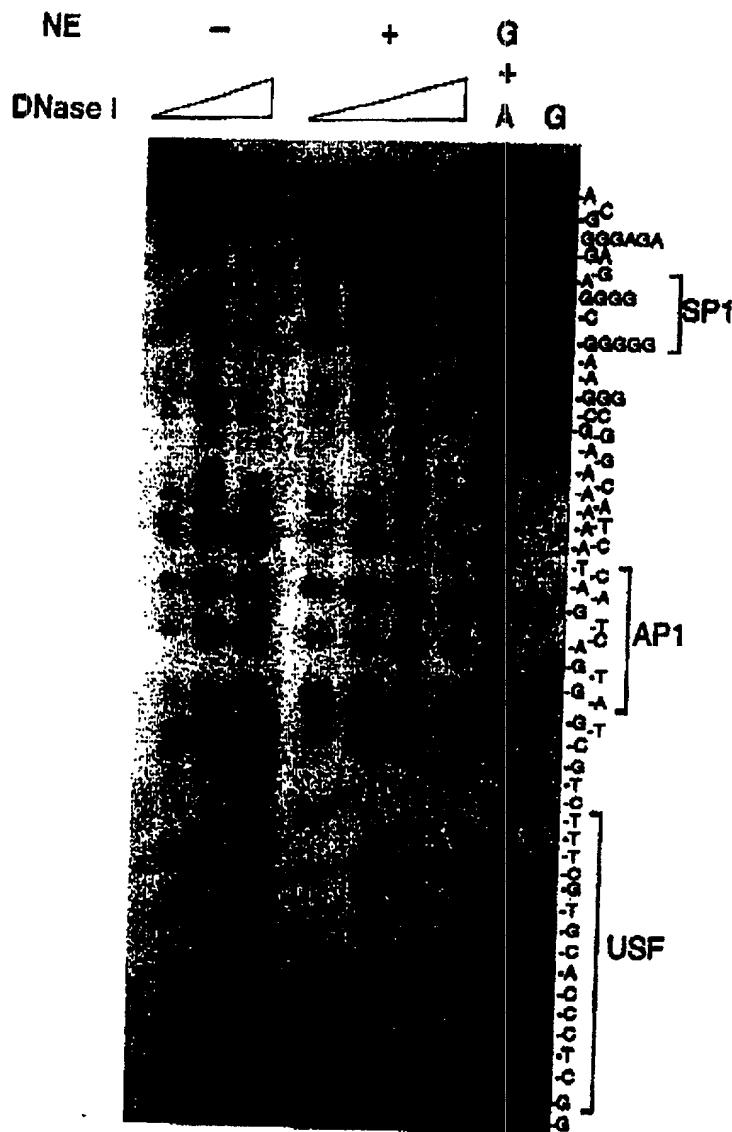


FIGURE 5



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FIGURE 6A

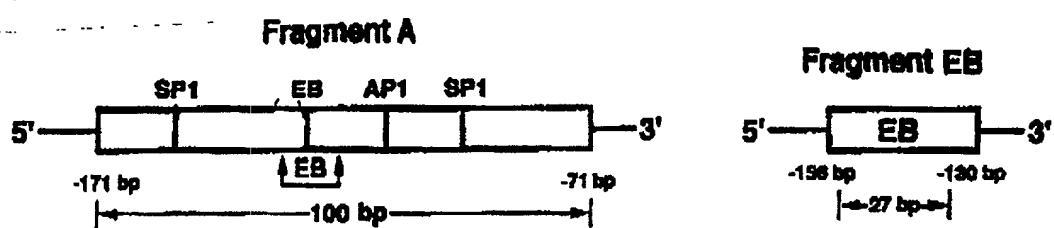
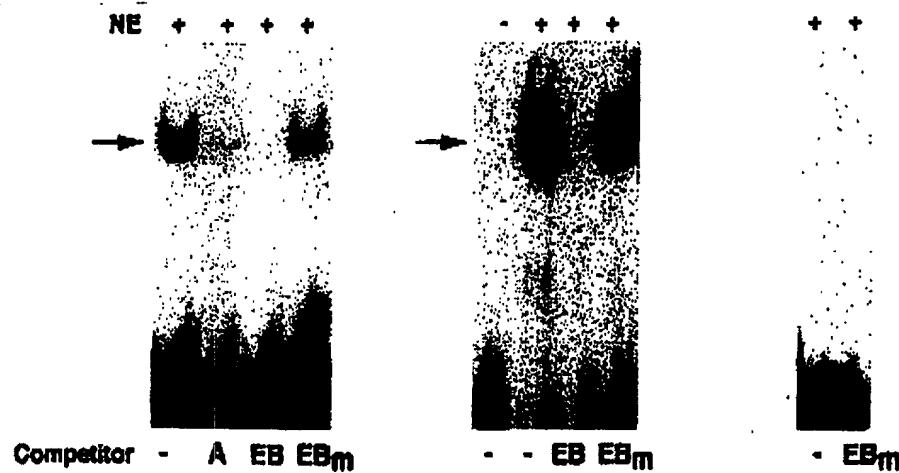


FIGURE 6B Fragment A



Fragment EB

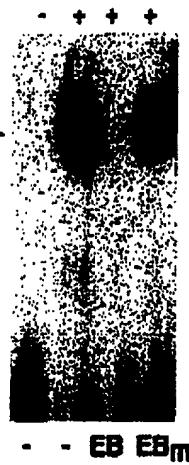
Fragment EB_m

FIGURE 6C

